```
              GenCore version 5.1.3
         Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:     February 16, 2003, 16:37:55 ; Search time 1441.15 Seconds
                                           (without alignments)
                                           15778.007 Million cell updates/sec

Title:           US-09-497-967-3
Perfect score:   1404
Sequence:        1 atgaaaaataatatttagt.........tgattcttattatttatta 1404

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:       32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
                 1:  em_estba:*
                 2:  em_esthum:*
                 3:  em_estin:*
                 4:  em_estmu:*
                 5:  em_estov:*
                 6:  em_estpl:*
                 7:  em_estro:*
                 8:  em_htc:*
                 9:  gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: gb_gss:*
                 18: em_gss_hum:*
                 19: em_gss_inv:*
                 20: em_gss_pln:*
                 21: em_gss_vrt:*
                 22: em_gss_fun:*
                 23: em_gss_mam:*
                 24: em_gss_mus:*
                 25: em_gss_other:*
                 26: em_gss_pro:*
                 27: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Match	Query Length	DB	ID	Description	
c	1	204.2	14.5	658	14	BQ135057	BQ135057	INIT1_2_G
c	2	199.8	14.2	607	14	BQ134912	BQ134912	INIT1_1_F
c	3	192.6	13.7	602	14	BQ135164	BQ135164	INIT1_4_B
c	4	191.6	13.6	590	14	BQ135179	BQ135179	INIT1_4_C
c	5	165.6	11.8	502	14	BQ134889	BQ134889	INIT1_1_D
c	6	159.4	11.4	445	14	BQ134871	BQ134871	INIT1_1_B
c	7	151.4	10.8	419	14	BQ135036	BQ135036	INIT1_2_D
c	8	134.4	9.6	675	14	BQ135196	BQ135196	INIT1_4_E
c	9	127.8	9.1	599	14	BQ134821	BQ134821	INIT1_4_D
c	10	115.2	8.2	540	14	BQ134879	BQ134879	INIT1_4_C
	11	113.8	8.1	538	14	BQ134810	BQ134810	INIT1_1_C
	12	110.4	7.9	630	14	BQ134905	BQ134905	INIT1_4_F
	13	110.4	7.9	631	14	BQ134827	BQ134827	INIT1_4_E
	14	109.4	7.8	523	14	BQ134970	BQ134970	INIT1_2_D
	15	106.4	7.6	514	14	BQ134761	BQ134761	INIT1_3_F
c	16	106.4	7.6	661	14	BQ135189	BQ135189	INIT1_4_D
	17	105.8	7.5	560	14	BQ135129	BQ135129	INIT1_3_F
	18	105.8	7.5	622	14	BQ134798	BQ134798	INIT1_4_B
	19	105.8	7.5	687	14	BQ135168	BQ135168	INIT1_4_B
c	20	103.2	7.4	337	14	BQ134748	BQ134748	INIT1_3_E
	21	99.2	7.1	592	14	BQ134985	BQ134985	INIT1_2_G
c	22	72.2	5.1	210	14	BQ134900	BQ134900	INIT1_1_E
	23	69.8	5.0	150	14	BQ135114	BQ135114	INIT1_3_E
	24	68.4	4.9	773	17	AL169549	CNS01VTG	Tetraodon
c	25	62		735	17	AL299119	CNS0NSM	Tetraodon
c	26	61.4	4.4	470	17	AL011359	FR0018463	F.rubripe
	27	61.4	4.4	989	17	AL197365	CNS02HA4	Tetraodon
	28	61.2	4.4	1101	17	AL063921	CNS0039G	Drosophil
	29	60.8	4.3	501	17	AL444958	FR0048173	Fugu rubr
	30	58.4	4.2	605	17	AZ640388	1M0502E21	
c	31	57.8	4.1	813	13	BJ406459	BJ406459	
	32	56.2	4.0	494	17	AL44858	FR0048073	Fugu rubr
	33	56.2	4.0	572	17	AL273200	CNS043SN	Tetraodon
	34	56.2	4.0	723	17	BH182027	BH182027	020_K.19-
c	35	56.2	4.0	723	17	AL618977	CNS07NIN	T3 end of
	36	56		824	17	AZ185454	AZ185454	SP_1005_A
	37	56		898	17	AZ282028	CNS04ALV	Tetraodon
	38	55.6	4.0	450	17	AL018519	FR0025683	F.rubripe
	39	55.4	3.9	623	9	AU060774	AU060774	
	40	55.4	3.9	742	17	AU060168	AU060168	
	41	55	3.9	619	17	Z90754	FR0006944	F.rubripes
c	42	55	3.9	805	17	AL304427	CNS04RW2	Tetraodon
	43	55	3.9	857	13	BJ403229	BJ403229	
c	44	55	3.9	1101	17	AL063921	CNS0039G	Drosophil
c	45	54.8	3.9	550	17	AL130699	FR0043207	Fugu rubr

ALIGNMENTS

```
RESULT 1
BQ135057/c
LOCUS       BQ135057               658 bp    mRNA    linear   EST 22-APR-2002
DEFINITION  INIT1_2_G01.g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
            multifiliis cDNA, mRNA sequence.
ACCESSION   BQ135057
VERSION     BQ135057.1  GI:20261156
KEYWORDS    EST.
SOURCE      Ichthyophthirius multifiliis.
ORGANISM    Ichthyophthirius multifiliis
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE   1  (bases 1 to 658)
AUTHORS     Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
            Dickerson,H. Lin,T.-L. and Pratt,L.H.
TITLE       An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL     Unpublished (2002)
COMMENT     Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector, and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Seq primer: T7
            High quality sequence start: 67
```

REFERENCE
AUTHORS   Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
           Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE   An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL   Unpublished (2002)
COMMENT   Contact: Cordonnier-Pratt MM
           Laboratory for Genomics and Bioinformatics
           The University of Georgia, Department of Plant Biology
           Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
           Tel: 706 542 1860
           Fax: 706 583 0210
           Email: mmpratt@uga.edu
           Sequences have been trimmed to exclude polyA, vector, and regions
           below Phred quality 16. The threshold for highest quality sequence
           is 20.
           Seq primer: JEN REV
           High quality sequence stop: 599
           POLYA=NO.

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases 1 to 607)

FEATURES   Location/Qualifiers
     source   1..607
                     /organism="Ichthyophthirius multifiliis"
                     /strain="G5"
                     /db_xref="taxon:5932"
                     /clone_lib="G5 trophont cDNA (INIT1)"
                     /note="Vector: pBluescript SK(-) from Lambda zap II;
                     Site_1: EcoRI; Site_2: EcoRI; The library was made from
                     trophont polyA+ RNA of the G5 parasite strain.
                     Double-stranded cDNA was linked to EcoRI adaptors, size
                     fractionated, and material >500 bp cloned into lambda ZAP
                     II. Plasmid DNA for sequencing was prepared by mass
                     excision."

BASE COUNT   199 a   111 c   104 g   193 t
ORIGIN

Query Match   14.2%;   Score 199.8; DB 14;   Length 607;
Best Local Similarity 65.6%; Pred. No. 2.8e-33;
Matches 377; Conservative 0; Mismatches 177; Indels 21; Gaps 5;

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Qy   841 AGTACATGCCTACCTTGCCCAGCAAATAAAGATTATGGTGCTGAAGCCACTGCAGGTGGT 900
             ||||| |  |||||||  ||||| |  ||||| || | |    |  |||||||||||||
Db   607 AGTAAATGCGTAGCTTGCGAATCAAAAAGACCAA---TTCTTAATCCAGATCAGGTCTT 551

Qy   901 GCCGCTACTTAGCCAAATAATGTAATATTGCATGCCCTGATGGTACTGCAATTGCTAGT 960
          | |||| |||||||  |||||||  |||| |||| || ||||| || |  ||||||||
Db   550 GAGGCTAATTTAGCCGCATAATGTGGCACTGAATGTCCTGCCACTCTTGTTACAGAC 491

Qy   961 GGAGCAA---CTAATTATGTAATAATTATTATAAACAGAATGTCTAAATTGTGCTGCTAACTTT 1017
          |||| ||   ||| ||  ||| |  | | ||| | | |||||| | |||||| |||  |||
Db   490 GGAGTAACCACCTACTTATACTGTATCATCTCATAATGTGTTAATTGTTAAAGCTGGCTTT 431

Qy  1018 TATTTTGATGGTAATAATTTCTAGGCAGGAAGTAGTAGATGAGACCAAAGCCATGTCCAGCAAAT 1077
          || | |   ||||| |||||||| |||| |   || |  |  |    | | | |||||||||||
Db   430 TACT---AAAATAGTAATTTCGAAGCAGGTAAAAGTTAATGCAATAAGTGTGCAGTAAGT 374

Qy  1078 AAAGTTTAAGGCGCTGAGCAACTGCAGGTGGTCAGCTGTCTACTTTAATTGCATAAATGTCGTACTTTAATTGCCGCC 1137
          |||| | ||| | | |  | |  |||| | | |||| || ||| ||  | |  |||| |||||
Db   373 AAAACT---GGTTCAGCATCTGTTCCAGGTAATAGTGCTACTTCAGCCACATAAATGTTAA 317

Qy  1138 CTTGAATGCCCTGCTGGTACTGTACTCACCGATGGAACAACATCTACTTATAAATAAGCA 1197
          | |||||||||||||||| || | | |  ||||| |||| |  |  ||  |||||||  |
Db   316 AACGATTGCCCTGCTGGTACAGTGGTTGATGATGGTACAACAACTAATTTTGTAGCTTTA 257

Qy  1198 GCAICTGAATGTGTTAAATGTCGTGCTGCCAACTTTTATACTACAAAATAAACTGATTGGGTA 1257
          |||  |||| ||| | ||| |  |  || | ||||||| | ||||| | |||| |  |||| |
Db   256 GCAAGTGAAGTGACTAAAGTGTTAGGCTAACTTTTATGCATCAAACAAAAACATCTGGTTTGCA 197

Qy  1258 GCAGGTATTGATACATGTACTAGTTGTAATAAAAATTAACTTCTGGCGCTGAAGCTAAT 1317
          ||||||| ||||| ||||||| |  || | |||||||||||||||| | | |||||||
Db   196 GCAGGTACTGATACATGTACTGAATGTTCTAAAAAAATTAACTTCTGGTACAGCTAAA 137

Qy  1318 TTACCTGAATCTGCTAAAAAAAATATATAAATGTG-------ATTTCGCTAATTTTTA 1368
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BASE COUNT   215 a   122 c   122 g   199 t
ORIGIN

High quality sequence stop: 658
POLYA=NO.

FEATURES   Location/Qualifiers
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                     /organism="Ichthyophthirius multifiliis"
                     /strain="G5"
                     /db_xref="taxon:5932"
                     /clone_lib="G5 trophont cDNA (INIT1)" from Lambda zap II;
                     /note="Vector: pBluescript SK(-) from Lambda zap II;
                     Site_1: EcoRI; Site_2: EcoRI; The library was made from
                     trophont polyA+ RNA of the G5 parasite strain.
                     Double-stranded cDNA was linked to EcoRI adaptors, size
                     fractionated, and material >500 bp cloned into lambda ZAP
                     II. Plasmid DNA for sequencing was prepared by mass
                     excision."

Query Match   14.5%;   Score 204.2; DB 14;   Length 658;
Best Local Similarity 65.0%; Pred. No. 3.1e-34;
Matches 388; Conservative 0; Mismatches 188; Indels 21; Gaps 5;

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Qy   819 TCCTAATTTCAATCCAGGTAATAGTACATGCCTACCTTGCCCAGCAAATAAAGATTATGG 878
Db   604 TCCTATGGTTCCTGGCCCTAATAGTAAATGCGTAGCTTGCGAATCAAAAAGACCAA--- 548

Qy   879 TGCTGAAGCCACTGCAGGTGGTGCCGCTACTTAGCCAAATAATGTAATATTGCATGCCCC 938
Db   547 TTCTTAATCCAGATCAGGTCTTGAGGCTAATTTAGCCGCATAATGTGGCACTGAATGTCC 488

Qy   939 TGATGGTACTGCAATTGCTAGTGGAG--CAACTAATTATGTAATAATTATTATAAACAGAATG 995
Db   487 TGCTGGCCACTCTTGTTACAGACGGAGTAACCACCTACTTATACTGTATCATCTCATAATG 428

Qy   996 TCTAAATTGTGCTGCTAACTTTTTATTTTGATGGTAATAATTTCTAGGCAGGAAGTAGTAG 1055
Db   427 TGTTAATTGTTAAAGCTGGCTTTTACT--AAAATAGTAATTTCGAAGCAGGTAAAAGTTA 371

Qy  1056 ATGAAAGCATGTCCAGCAAATAAAGTTTAAGGCGCTGAGCAACTGCAGGTGGTCAGCTGC 1115
Db   370 ATGCAATAAGTGTGCAGTAAGTAAAACT--GGTTCAGCATCTGTTCCAGGTAATAGTGC 314

Qy  1116 TACTTTAATTGCATAAATGTCGTACCCTGCTGGTACTGTACTCACCGATGGAAC 1175
Db   313 TACTTCAGCCACATAAATGTTAAAACGATTGCCCTGGTACAGTGGTTGATGATGGTAC 254

Qy  1176 AACATCTACTTATAAATAAGCAGCAGTCATCTGAATGTGTTAAATGTCGTGCTGCCAACTTTTATAC 1235
Db   253 ATCAACTAATTTTGTAGCTTTAGCAAGTGAATGTACTAAATGTTCTAAACTTTTATGC 194

Qy  1236 TACAAAATAAACTGATTGGGTAGCAGGTATTGATACATGTACTAGTTGTAATAAAAATT 1295
Db   193 ATCAAAAACATCTGGTTTGCAGCAGGTACTGATACATGTACTGAATGTTCTAAAAAAATT 134

Qy  1296 AACTTCTGGCGCTGAAGCTAATTTACCTGAATCTGCTAAAAAAAATATATAAATGTG---- 1351
Db   133 AACTTCTGGTACAGCTAAAGTATATGCTGAAGCTACTAAAAGCATAAATGCGGCCAG 74

Qy  1352 -----ATTTCGCTAATTTTTATCAATTTCCTTATTATTGATTTCTTATTATTTATT 1403
Db    73 TTCCACTTTCGCAAAATTTTATCAATGTCCTTAAATATTTTATTTCTTTCTATTGTT 17
```

RESULT 2
BQ134912/c
LOCUS   BQ134912   607 bp   mRNA   linear   EST 22-APR-2002
DEFINITION INIT1_F12.b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
            multifiliis cDNA, mRNA sequence.
ACCESSION   BQ134912
VERSION   BQ134912.1 GI:20261011
KEYWORDS   EST.
SOURCE   Ichthyophthirius multifiliis
ORGANISM   Ichthyophthirius multifiliis

```
Db   136  GTATATGCTGAAGCTACTTAAAAAGCATAATGCGCCAGTTCCACTTTCGCAAAATTTTA 77
          ||   ||||||     |||| ||||   |||||| || |||||||
Qy  1369  TCAATTTCCTTATTATTGATTTCTTATTATTTATT 1403
          |||| |||||| |||  ||||||  |||| ||
Db    76  TCAATGTCCTTAATATTTATTTCTTTCTATTTGTT 42
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```
RESULT 3
BQ135164/c
LOCUS       BQ135164              602 bp    mRNA    linear  EST 22-APR-2002
DEFINITION  INIT1_4_B05.g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
            multifiliis cDNA, mRNA sequence.
ACCESSION   BQ135164
VERSION     BQ135164.1  GI:20261263
KEYWORDS    EST.
SOURCE      Ichthyophthirius multifiliis.
ORGANISM    Ichthyophthirius multifiliis
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE   1  (bases 1 to 602)
AUTHORS     Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
            Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE       An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL     Unpublished (2002)
COMMENT     Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector, and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Double-stranded cDNA was linked to EcoRI adaptors, size
            fractionated, and material >500 bp cloned into lambda ZAP
            II. Plasmid DNA for sequencing was prepared by mass
            excision."
            Seq primer: T7
            High quality sequence start: 3
            High quality sequence stop: 602
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1..602
                     /organism="Ichthyophthirius multifiliis"
                     /strain="G5"
                     /db_xref="taxon:5932"
                     /clone_lib="G5 trophont cDNA (INIT1)"
                     /note="vector: pBluescript SK(-) from Lambda Zap II;
                     Site_1: EcoRI; Site_2: EcoRI; The library was made from
                     trophont polyA+ RNA of the G5 parasite strain.
                     Double-stranded cDNA was linked to EcoRI adaptors, size
                     fractionated, and material >500 bp cloned into lambda ZAP
                     II. Plasmid DNA for sequencing was prepared by mass
                     excision."
BASE COUNT      214 a    103 c     92 g    193 t
ORIGIN
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Query Match          13.7%;    Score 192.6;  DB 14;  Length 602;
Best Local Similarity 66.2%;    Pred. No. 1e-31;
Matches  346;  Conservative   0;  Mismatches 159;  Indels  18;  Gaps   4;
```

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Qy   893  CAGGTGGTGCCGCCTACTTTAGCCAAATAATGTAATATTGCATGCCCTGATGCTACTGCAA 952
          ||||| || |||| ||||||||  ||| ||| |||| |||| | ||| || |||||||
Db   599  CAGGTCTGAGCGTAATTTAGCCGCATAAATGTGGCACTGAATGTCCTGGCACTCTTG 540
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```
Qy   953  TTGCTAGTGGGAGCAA---CTAATTATGTAATATTATAAACAGAATGTCTAAATTGTCTG 1009
          || |    ||| || |     |||  ||| |||| |||| ||  ||||| ||| |||
Db   539  TTACAGACGGAGTAACACCTACTTATACTGTATCATCTCATAAATGTGTTAATTGTAAAG 480
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```
Qy  1010  CTAACTTTATTTTGATGGTAATAATTTCTTAGGCAGGAAGTAGATGCAAAGCATGTC 1069
          ||  |||||  |  |||  ||||    | |||||| | |||||  |   |||||
Db   479  CTGGCTTTTACTAAAA---TAGTAATTTCGAAGCAGTAGATGCTACTTAATTGCAT 423
```

```
Qy  1070  CAGCAAATAAAGTTTAAGGCCTGTAGCAACTGCAGGTGGTACTGCTACTTTAATTGCAT 1129
          ||| || |||| || |  |  |||||||| ||  |||||| ||| || ||||| ||| ||
```

```
Db   422  CAGTAAGTAAAACT---GGTTCAGCATCTGTTCCAGGTAATAGTGCTACTTCAGCCACAT 366
          ||||                 ||||||||||| | || ||  |||||| || ||| |
Qy  1130  AATGTGCCCTTGAATGCCCTGCTGCTGGTACTCTCACCGATGGAACAAACATCTACTTATA 1189
          |||||      ||| ||  |||||||||| ||  || ||| || |||||  ||||||
Db   365  AATGTTAAAACGATTGCCCTGCTGGTACAGTGGTTGATGATGGTACATCAACTAATTTTG 306
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```
Qy  1190  AATAAGCAGCATCTGAATGTGTTAAATGTCTGCCAACTTTTATATCTACAAAATAAACTG 1249
          |    |||| |||||   |||||| ||   |||| |||| |  |||  ||||| |||
Db   305  TAGCTTTAGCAAGTGAATGTACTAAATGTTAGGCTAACTTTTATGCATCAAAAACATCTG 246
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```
Qy  1250  ATTGGGTAGCAGGTATTGATACATGTACTAGTTGTAATAAAAATTAACTTCTGCGCGTG 1309
          |||       ||| ||  || |||||| | ||||| ||||||| | |||||||||||||
Db   245  GTTTTGCAGCAGGTACTGAATACATGTACTGAAGTTCTAAAAATTAACTTCTGCGTGCTA 186
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```
Qy  1310  AAGCTAATTTACCTGAATCTGCTAAAAAAAATATATAATGTG------ATTTCGCTA 1360
          ||| |||| ||| |||| || |||||||||||||||||||        |||||||
Db   185  CAGCTAAAGTATATGCTGAAGCTACTTAAAAAGCATAATGCGCCAGTTCCACTTTCGCAA 126
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```
Qy  1361  ATTTTTTATCAATTTCCTTATTATTGATTTCTTATTATTTATT 1403
          |||||||||||| |||  ||||||  |||| ||
Db   125  AATTTTTATCAATGTCCTTAATATTTATTTCTTTCTATTTGTT 83
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```
RESULT 4
BQ135179/c
LOCUS       BQ135179              590 bp    mRNA    linear  EST 22-APR-2002
DEFINITION  INIT1_4_C08.g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
            multifiliis cDNA, mRNA sequence.
ACCESSION   BQ135179
VERSION     BQ135179.1  GI:20261278
KEYWORDS    EST.
SOURCE      Ichthyophthirius multifiliis.
ORGANISM    Ichthyophthirius multifiliis
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE   1  (bases 1 to 590)
AUTHORS     Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
            Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE       An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL     Unpublished (2002)
COMMENT     Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector, and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Seq primer: T7
            High quality sequence start: 43
            High quality sequence stop: 590
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1..590
                     /organism="Ichthyophthirius multifiliis"
                     /strain="G5"
                     /db_xref="taxon:5932"
                     /clone_lib="G5 trophont cDNA (INIT1)"
                     /note="vector: pBluescript SK(-) from Lambda zap II;
                     Site_1: EcoRI; Site_2: EcoRI; The library was made from
                     trophont polyA+ RNA of the G5 parasite strain.
                     Double-stranded cDNA was linked to EcoRI adaptors, size
                     fractionated, and material >500 bp cloned into lambda ZAP
                     II. Plasmid DNA for sequencing was prepared by mass
                     excision."
BASE COUNT      207 a    103 c     94 g    186 t
ORIGIN
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Query Match          13.6%;    Score 191.6;  DB 14;  Length 590;
Best Local Similarity 66.1%;    Pred. No. 1.7e-31;
Matches  345;  Conservative   0;  Mismatches 159;  Indels  18;  Gaps   4;
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                                                          /clone_lib="G5 trophont cDNA (INIT1)"
                                                          /note="vector: pBluescript SK(-) from Lambda zap II;
                                                          Site_1: EcoRI; Site_2: EcoRI; The library was made from
                                                          trophont polyA+ RNA of the G5 parasite strain.
                                                          Double-stranded cDNA was linked to EcoRI adaptors, size
                                                          fractionated, and material >500 bp cloned into lambda ZAP
                                                          II. Plasmid DNA for sequencing was prepared by mass
                                                          excision."
BASE COUNT      185 a        80 c        70 g       167 t
ORIGIN

Query Match                 11.8%;    Score 165.6; DB 14;   Length 502;
Best Local Similarity       67.2%;    Pred. No. 7.5e-26;
Matches  285;   Conservative    0;   Mismatches  124;   Indels  15;   Gaps   3;

Qy     989 CAGAATGTCTAAATTGTCTGCTAACTTTTATTTGATGGTAATAATTTCTAGGCAGGAA 1048
           || ||||| |||| ||||||||||||  ||| ||||| | |||||||| ||||||||
Db     498 CATAATGTGTTAATTGTAAAGCTGGCTTTTACT----AAAATAGTAATTTCGAAGCAGGTA 442

Qy    1049 GTAGTAGATGCAAAGCATGTCCAGCAAATAAAGTTAAGGCCGTGTAGCAACTGCGAGGTG 1108
           || |||||| ||||   ||||||||||||  ||| | || ||||| | ||||||
Db     441 AAAGTTAATGCAATAAGTGTGCAGTAAGTAAAACT---GGTTCAGCATCTGTTCCAGGTA 385

Qy    1109 GTACTGCTACTTTAATTGCATAATGTGCCCTTGCTGCTCGGTGACTGCTACTCACCG 1168
           | |||||||| ||||||||||||   || ||||||||||||| || ||||
Db     384 ATAGTGCTACTTGCAGCCACCATAATGTTTAAAACGATTGCCCTGCTGGTGACAGTGGTTGATG 325

Qy    1169 ATGGAACAACATCTACTTTATAATAAGCAGCATCTGAATGTGTTAAATGTGCTGCCAACT 1228
           ||| ||||||||||||| |||||  ||||| |||||||||||||||| | |||
Db     324 ATGGTACATCAACTAATTTTGTAGCTTTAGCAAGTGAAGTGTACTAAATGTTAGGCTAACT 265

Qy    1229 TTTATACTACAAAATAAACTGATTGGGTAGCAGGTAATGTTGATACATGTACTAGTTGTAATA 1288
           ||||| ||||| || ||| | ||||||||||||| ||||||||  ||||||
Db     264 TTTATGCATCAAAAACATCTGGTTTCAGCAGCTACTGATACATGTACTGATAGTGTTCTA 205

Qy    1289 AAAAATTAACTTCTGGCGTGAAGCTAATTTACCTGAATCTGCTAAAAAAAATATATAAT 1348
           ||||||||||||||||| || || |||||||||| ||||| || ||||
Db     204 AAAAATTAACTTCTGTGTGCTACAGCTAAAGTATATGCTGAAGCTACTTAAAAGCATAAT 145

Qy    1349 GTG--------ATTTCGCTAATTTTTTATCAATTTCCTTATTATTGATTTCTTATTATT 1399
                     |||||||||||||||| || | |||||||||||| ||||||||||||||
Db     144 GCGCCAGTTCCACTTTCGCAAAAATTTTTATCAATGTCCTTAATATTTATTTCTTTCTATT 85

Qy    1400 TATT 1403
           | ||
Db      84 TGTT 81


RESULT 6
BQ134871/c
LOCUS          BQ134871          445 bp    mRNA    linear    EST 22-APR-2002
DEFINITION     INIT1_B05.b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
               multifiliis cDNA, mRNA sequence.
ACCESSION      BQ134871
VERSION        BQ134871.1  GI:20260970
KEYWORDS       EST.
SOURCE         Ichthyophthirius multifiliis.
ORGANISM       Ichthyophthirius multifiliis
               Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
               Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE      1 (bases 1 to 445)
AUTHORS        Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
               Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE          An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL        Unpublished (2002)
COMMENT        Contact: Cordonnier-Pratt MM
               Laboratory for Genomics and Bioinformatics
               The University of Georgia, Department of Plant Biology
               Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
               Tel: 706 542 1860
               Fax: 706 583 0210
               Email: mmpratt@uga.edu
               Sequences have been trimmed to exclude PolyA, vector, and regions
```

```
Qy     894 AGGTGGTGCCGCTACTTTAGCCAAATAATGTAATATTGCATGCCCTGATGGTACTGCAAT 953
           |||| || |||| |||||| ||||||||  ||||  |  |  |  ||| ||||| || |
Db     590 AGGTCTTGAGGCTAATTTAGCCGCATAAATGTGGCACTGAATGTCCGCTGGCACTCTTGT 531

Qy     954 TGCTAGTGGAGCAA---CTAATTATGTAATATTATAAACAGAATGTCTAAATTGTGCTGC 1010
           || | |||| ||||   | |   ||  | || || ||  |||  ||||||||| |||||
Db     530 TACAGACGGAGTAACACCTACTTATACTGTATCACTCTCATAATGTGTTAATTGTAAAGC 471

Qy    1011 TAACTTTTATTTGATGGTAATAATTTCTAGGCAGGAAGTAGTAGATGCAAAGCATGTCC 1070
           | ||||| |  |||||||| ||||||| ||||| ||  ||||||  |
Db     470 TGGCTTTTACTAAAA---TAGTAATTTCGAAGCAGGTAAAAGTTAATGCAATAAGTGTGC 414

Qy    1071 AGCAAATAAAGTTAAGGCCGTGTAGCAACTGCAGGTGGTACTGCTACTTTAATTGCATA 1130
           || || |  || | | |  ||   || | | |||| ||| | |||||||| |||||
Db     413 AGTAAGTAAAACT---GGTTCAGCATCTGTTCCAGCTAATAGTGCTACTTGCAGCCACACA 357

Qy    1131 ATGTGCCCTTGAATGCCCTGCTGGTACTGTACTCACCGATGGAACAACATCTACTTATAA 1190
           |||| ||   | ||||| ||||| ||||| | |||||||
Db     356 ATGTTAAAACGATTGCCCTGCTGGTACAGTGGTTGATGATTCAACTAATTTTGT 297

Qy    1191 ATAAGCAGCATCTGAATGTGTTAAATGTGCTCGCCAACTTTTATACTACAAAATAAACTGA 1250
           | |||| |||||||||||| ||||| ||   || | | |  |  |  ||
Db     296 AGCTTTAGCAAGTGAATTGAATGTACTTTTATGCATCAAAAACATCTGG 237

Qy    1251 TTGGGTAGCAGGTATTGATACATGTACTAGTTGTAATAAAAAAATATAATGTG------- 1310
           || | |||||||| ||||||||||||| ||  ||||||||||| ||||||
Db     236 TTTTGCAGCAGGTACTGATACATGTACTGATAGTGTTCTGGTGTGCTAC 177

Qy    1311 AGCTAATTTACCTGAATCTGCTAAAAAAAATATAATGTG-------ATTTCGCTAA 1361
           || ||||||||||||||| ||||||  |||||||||||       ||||||||||
Db     176 AGCTAAAGTATATGCTGAAGCTACTTAAAAGCATAAATGCGCCAGTTCCACTTTCGCAAA 117

Qy    1362 TTTTTTATCAATTTCCTTATTATTGATTTCTTATTATT 1403
           |||||  ||||| |||||| ||||| ||||||| | ||
Db     116 ATTTTTATCAATGTCCTTAATATTTATTTCTTTCTGTT 75


RESULT 5
BQ134889/c
LOCUS          BQ134889          502 bp    mRNA    linear    EST 22-APR-2002
DEFINITION     INIT1_1_D07.b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
               multifiliis cDNA, mRNA sequence.
ACCESSION      BQ134889
VERSION        BQ134889.1  GI:20260988
KEYWORDS       EST.
SOURCE         Ichthyophthirius multifiliis.
ORGANISM       Ichthyophthirius multifiliis
               Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
               Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE      1 (bases 1 to 502)
AUTHORS        Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
               Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE          An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL        Unpublished (2002)
COMMENT        Contact: Cordonnier-Pratt MM
               Laboratory for Genomics and Bioinformatics
               The University of Georgia, Department of Plant Biology
               Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
               Tel: 706 542 1860
               Fax: 706 583 0210
               Email: mmpratt@uga.edu
               Sequences have been trimmed to exclude PolyA, vector, and regions
               below Phred quality 16. The threshold for highest quality sequence
               is 20.
               Seq primer: JEN REV
               High quality sequence stop: 474
               POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1..502
                     /organism="Ichthyophthirius multifiliis"
                     /strain="G5"
                     /db_xref="taxon:5932"
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```
TITLE      An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL    Unpublished (2002)
COMMENT    Dickerson,H., Lin,T.-L. and Pratt,L.H.
           Contact: Cordonnier-Pratt MM
           Laboratory for Genomics and Bioinformatics
           The University of Georgia, Department of Plant Biology
           Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
           Tel: 706 542 1860
           Fax: 706 583 0210
           Email: mmpratt@uga.edu
           Sequences have been trimmed to exclude PolyA, vector, and regions
           below Phred quality 16. The threshold for highest quality sequence
           is 20.
           Seq primer: T7
           High quality sequence start: 306
           High quality sequence stop: 419
           POLYA=yes.
FEATURES             Location/Qualifiers
     source          1..419
                     /organism="Ichthyophthirius multifiliis"
                     /strain="G5"
                     /db_xref="taxon:5932"
                     /clone_lib="G5 trophont cDNA (INIT1)"
                     /note="Vector: pBluescript SK(-) from Lambda zap II;
                     Site_1: EcoRI; Site_2: EcoRI; The library was made from
                     trophont polyA+ RNA of the G5 parasite strain.
                     Double-stranded cDNA was linked to EcoRI adaptors, size
                     fractionated, and material >500 bp cloned into lambda ZAP
                     II. Plasmid DNA for sequencing was prepared by mass
                     excision."
BASE COUNT      140 a     74 c     73 g    132 t
ORIGIN

Query Match    10.8%;  Score 151.4;  DB 14;  Length 419;
Best Local Similarity   66.4%;  Pred. No. 9.2e-23;
Matches 253;  Conservative   0;  Mismatches 116;  Indels  12;  Gaps   2;

Qy   1032  TAATTTCTAGGCAGGAAGTAGTAGAGATGCAAAGCATGTCCAGCAAATAAAGTTTAAGGCGC   1091
           ||||||| | |||||| |   |||||| ||||||||||||| ||||||||||||||||
Db    411  TAATTTCGAAGCAGGTAAAAGTTAATGCAACAAGTGCAGTAAGTAAGTAAAACT---GGTTC    355

Qy   1092  TGTAGCAACTGCAGGTGGTACTGCTACTTTAATTGCATAATGTCCCTTGAATGTGCCCTGC   1151
           | ||||  ||| |||| ||||| |||||||| || ||||||||| ||||| ||||| |||
Db    354  AGCATCTGTTCCAGGTAATAGTGTACTCACTTCAGCCACCACATAATGTTAAAACGATTGCC   295

Qy   1152  TGGTACTGTACTCACCGATGGAACAACATCTACTTATAATAAATAAGCAGCATCTGAATGTGT   1211
           ||||| ||  |||| ||| |||||||||| |||||| |||||| ||||| |||||
Db    294  TGGTACAGTGGTTGATGATGGTTCATCAACTAATTTTGTAGCTTTAGCAAGTGAATGTAC    235

Qy   1212  TAAATGTGCTGCCAACTTTTATACTACAAAATAAACTGATTGGGTAGCAGGTATTGATAC   1271
           ||||||| | ||||| |||||  ||||||||| |  ||||| | |||||| |||||||
Db    234  TAAATGTTAGGCTAACTTTTATGCATCAAAAACATCTGGTTTCGGCAGCAGGTACTGATCC    175

Qy   1272  ATGTACTAGTTGTAATAAAAAAATTAACTTCTGGCCGTGAAGCTAATTTACCTGAATCTGC   1331
           ||||||  ||||| || ||||||||||||||| ||| |||  | |||  ||||||||||
Db    174  ATGTACTGAATGTTTTAAAAAATTAACTTCCGGTGCTACAGCTAAAGTATACGCGGAAGC    115

Qy   1332  TAAAAAAAATATATAATGTG--------ATTTCGCTAATTTTTATCAATTTCCTTATT   1382
           || |||  ||||  |  | |         |||||| ||||||||||||||||||||||
Db    114  TACTTAAAAGCATAATGCGCCCAGTTCCACTTTCGCAAATTTTTATCAATGTCCCTTAAT     55

Qy   1383  ATTGATTTCTTATTATTTATT   1403
           ||| || |||| ||| | |||
Db     54  ATTTATTTCTTTCTATTTGTT     34
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RESULT 8
```
BQ135196/c
LOCUS       BQ135196                 675 bp    mRNA    linear   EST 22-APR-2002
DEFINITION  INIT1_4_E06.g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
            multifiliis cDNA, mRNA sequence.
ACCESSION   BQ135196
VERSION     BQ135196.1  GI:20261295
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           below Phred quality 16. The threshold for highest quality sequence
           is 20.
           Seq primer: JEN REV
           High quality sequence start: 37
           High quality sequence stop: 443
           POLYA=yes.
FEATURES             Location/Qualifiers
     source          1..445
                     /organism="Ichthyophthirius multifiliis"
                     /strain="G5"
                     /db_xref="taxon:5932"
                     /clone_lib="G5 trophont cDNA (INIT1)"
                     /note="Vector: pBluescript SK(-) from Lambda zap II;
                     Site_1: EcoRI; Site_2: EcoRI; The library was made from
                     trophont polyA+ RNA of the G5 parasite strain.
                     Double-stranded cDNA was linked to EcoRI adaptors, size
                     fractionated, and material >500 bp cloned into lambda ZAP
                     II. Plasmid DNA for sequencing was prepared by mass
                     excision."
BASE COUNT      155 a     79 c     71 g    140 t
ORIGIN

Query Match    11.4%;  Score 159.4;  DB 14;  Length 445;
Best Local Similarity   66.5%;  Pred. No. 1.7e-24;
Matches 280;  Conservative   0;  Mismatches 126;  Indels  15;  Gaps   3;

Qy    989  CAGAATGTCTAAATTGTGCTGCTAACTTTTATTTGATGGTAATAATTCTAGGCAGGAA   1048
           || ||||| || | ||| |   ||||||||||| | | ||||||| || |||||||||
Db    442  CATAATGTTGTTACTTGTAAAGCTGGCTTTTACT---AAAATAGTAATTTCGAAGCAGGTA    386

Qy   1049  GTAGTAGATGCAAAGCATGTCCAGCAAATAAAGTTTAAGGCCCTGCAGCAACTGCAGGTG   1108
           | || |||  ||| | ||||  || |||||| ||||  ||  ||| | |||  |||| ||
Db    385  AAAGTTAATGCAATAAGTGTGCAGTAAGTAAAACT---GGTTCAGCATCTGTTCCAGGTA    329

Qy   1109  GTACTGCTACTTTAATTGCATAAATGTGCCCTTGAATGTCGTACTTGCTACTCACCG   1168
           ||| |||||| ||  |||| || |  |||| || ||  |  |||| | |  || |||
Db    328  ATAGTGCTACTTCAGCCACCATAATGTTAAAACGATTGCCCTGCTGGTACGTGGTTGATG    269

Qy   1169  ATGGAACAACATCTACTTATAAATAAGCAGCATCTGAATGTGTTAAATGTGCTGCCAACT   1228
           ||||  |||| || || |||  | ||||| | ||| |||  ||| ||||  | ||||||
Db    268  ATGGTTCATCAACTAATTTTGTAGCTTTAGCAAGTGAATGTCCTAAATGTTAGGCTAACT    209

Qy   1229  TTTATACTACAAAATAAACTGATTGGGTAGCAGGTATTGATACATGTACTAGTTGTAATA   1288
           |||||  |||||||| || ||||| |  | ||| | |||||| ||| | ||||  | ||
Db    208  TTTATGCATCAAAAACATCTGGTTTTGCGTTGTTTGCAGCAGGTACTGATACATTGTTCTA    149

Qy   1289  AAAAATTAACTTCTGGCCGTGAAGCTAATTTACCTGAATCTGCTAAAAAAAATATATAAT   1348
           ||||||||||||  || ||  | |  | | |  |||| | |   |||| || ||||| ||
Db    148  AAAAATTAACTTTTGGTGCTACAGTGTATGTTGCTGAAGCTATATGTCAAGCTACTTAAAAAGCATAAT     89

Qy   1349  GTG--------ATTTCGCTAATTTTTATCAATTTCCTTATTATTGATTTCTTATTATT   1399
            |          |||||| ||||||||||||||||||||  |||||| |||| |||
Db     88  GCGCCCAGTTCCACTTTCGCAAATTTTTATCAATGTCCTTAATATTTATTTATTTCTTTCTATT     29

Qy   1400  T   1400
           |
Db     28  T     28
```

RESULT 7
```
BQ135036/c
LOCUS       BQ135036                 419 bp    mRNA    linear   EST 22-APR-2002
DEFINITION  INIT1_2_D10.g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
            multifiliis cDNA, mRNA sequence.
ACCESSION   BQ135036
VERSION     BQ135036.1  GI:20261135
KEYWORDS    EST.
SOURCE      Ichthyophthirius multifiliis
  ORGANISM  Ichthyophthirius multifiliis
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE   1  (bases 1 to 419)
  AUTHORS   Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
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KEYWORDS    EST.
SOURCE      Ichthyophthirius multifiliis.
ORGANISM    Ichthyophthirius multifiliis
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE   1 (bases 1 to 675)
AUTHORS     Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
            Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE       An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL     Unpublished (2002)
COMMENT     Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector, and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Seq primer: T7
            High quality sequence start: 42
            High quality sequence stop: 675
            POLYA=NO.
FEATURES    Location/Qualifiers
     source 1..675
            /organism="Ichthyophthirius multifiliis"
            /strain="G5"
            /db_xref="taxon:5932"
            /clone_lib="G5 trophont cDNA (INIT1)"
            /note="Vector: pBluescript SK(-) from Lambda Zap II;
            Site_1: EcoRI; Site_2: EcoRI; The library was made from
            trophont polyA+ RNA of the G5 parasite strain.
            Double-stranded cDNA was linked to EcoRI adaptors, size
            fractionated and material >500 bp cloned into lambda ZAP
            II. Plasmid DNA for sequencing was prepared by mass
            excision."
BASE COUNT     216 a   126 c   127 g   206 t
ORIGIN

Query Match            9.6%;  Score 134.4;  DB 14;  Length 675;
Best Local Similarity  63.3%;  Pred. No. 4.6e-19;
Matches 291:  Conservative   0;  Mismatches 156;  Indels  13;  Gaps   5;

Qy    819 TCCTAATTTCAATCCAGGTAATAGTACATGCCTACCTTGCCCAGCAAATAAAGATTATGG  878
          ||||  |     ||||||| ||  ||||||| |||| || |||| |||| || | |||
Db    459 TCCTATGGTTCCTGGCCCTAATAGTAAATGCGTAGCTTGCGAATCAAAAAAGACCAA---  403

Qy    879 TGCTGAAGCCACTGCAGGTGGTGCCGCTACTTTAGCCAAATAATGTAATATTGCATGCCC  938
          | ||  |||||  ||||| ||  ||| ||||| |||||| |    |  || ||| || ||
Db    402 TTCTTAATCCAGATCAGGTCTTGAGGCTAATTTAGCCGCATAATGTGGCACTGAATGTCC  343

Qy    939 TGATGGTACTGCAATTGCTAGTGGAG---CAACTAATTATGTAATATTATAAACAGAATG  995
          |   || || ||  |      |||||   |||| |||| | |||| ||| ||||| ||||
Db    342 TGCTGGCACTCTTGTTACAGACGGAGTAAACAGATTTATTTGATGGTAATAAATTCTAGG  283

Qy    996 TCTAAATTGCTGCTAACTTTATTTGTAATAATTTCTAGGCAGGAGTAGTAG         1055
          | |||| | |||| ||||| | |||||| |||| |||||| ||| ||
Db    282 TGTTAATTGTAAAGCTGGCTTTTACT--AAAATAGTAATTTCGAAGCAGGTAAAAGTTA   226

Qy   1056 ATGCAAAGCATGTCCAGCAAATAAAGTTTAAGGCGCTGTAGCAACTGCAGGTGGTACTGC  1115
          ||||||| ||     |||||||||||||| || |||  |||| ||  | ||| ||
Db    225 ATGCAATAAGTGTGCAGTAAGTAAAACT---GGTTCAGCCATCTGTTCCAGGTAATAGTGC  169

Qy   1116 TACTTTAATTGCATAATGTGCCCTTGAATGCCCTGCTACTGTACTCACCGATGGAAC    1175
          | |||| |||| ||||||   |||| ||||||||||| ||||| || | |
Db    168 TACTTCAGCCACCATAATGTTAAAACGATTGCCCTGCTGGTTGCTACAGTGGTTACG    109

Qy   1176 AACATCTACTTATAAATAAGCACAGCATCTGAATGTGTTAAATGCGTCGCCCAACTTTTATAC  1235
          | | ||| || |  | || ||| ||   |  ||| || ||||| | |||||| ||||||
Db    108 ATCAACTAATTTTGTACCAAGTGAATGTACTAAATGTTAGGCTTAAGGTCTAACTTTTTATGC   49

Qy   1236 TACAAAAATAAACTGATTGGGTAG-CAGGTATTGATACACG  1274
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Qy  1116  TACTTTAATTGCATAATGTGCCCTTGAATGCCCGCTGGTACTGTGTACTCACCGATGGAAC  1175
               ||||| ||||||||  |||| |||||||||| ||  ||  ||    |||||| ||
Db   140  TACTTTCAGCCACATAATGTTAAAACGATTGCCCCTGCTGCTGGTACAGTGGTTGATGGTAC  81

Qy  1176  AACATCTACTTATATAAATAAGCAGCATCTGAATGTGTTAAATGTGCTGCCAACTTTTATAC  1235
               |  |||||||-|-| |||| |||||  |||  ||| ||||||| |||||||
Db    80  ATCAACTAATTTTGTAGCTTTAGCAAGTGAATGTACTCAAATGTTAGGCTAACTTTTATGC  21

Qy  1236  TACAAAA  1242
               |||||
Db    20  ATCAAAA  14
```

RESULT 10
BQ134879
LOCUS   BQ134879   540 bp   mRNA   linear   EST 22-APR-2002
DEFINITION INIT1_1_C04.b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
           multifiliis cDNA, mRNA sequence.
ACCESSION BQ134879
VERSION   BQ134879.1 GI:20260978
KEYWORDS   EST.
SOURCE   Ichthyophthirius multifiliis.
ORGANISM   Ichthyophthirius multifiliis
           Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
           Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE 1 (bases 1 to 540)
AUTHORS   Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
           Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE   An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL   Unpublished (2002)
COMMENT   Contact: Cordonnier-Pratt MM
           Laboratory for Genomics and Bioinformatics
           The University of Georgia, Department of Plant Biology
           Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
           Tel: 706 542 1860
           Fax: 706 583 0210
           Email: mmpratt@uga.edu
           Sequences have been trimmed to exclude PolyA, vector, and regions
           below Phred quality 16. The threshold for highest quality sequence
           is 20.
           Seq primer: JEN REV
           High quality sequence stop: 449
           POLYA=No.
FEATURES   Location/Qualifiers
     source   1..540
                    /organism="Ichthyophthirius multifiliis"
                    /strain="G5"
                    /db_xref="taxon:5932"
                    /clone_lib="G5 trophont cDNA (INIT1)"
                    /note="Vector: pBluescript SK(-) from Lambda zap II;
                    Site_1: EcoRI; Site_2: EcoRI; The library was made from
                    trophont polyA+ RNA of the G5 parasite strain.
                    Double-stranded cDNA was linked to EcoRI adaptors, size
                    fractionated, and material >500 bp cloned into lambda ZAP
                    II. Plasmid DNA for sequencing was prepared by mass
                    excision."
BASE COUNT   163 a   97 c   97 g   183 t
ORIGIN

Query Match   8.2%; Score 115.2; DB 14; Length 540;
Best Local Similarity 60.0%; Pred. No. 6.8e-15;
Matches 245; Conservative   0; Mismatches 133; Indels 30; Gaps 2;

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Qy    1  ATGAAAAATAATATTTTAGTAATATTGATTATTTCATTATTTATTCAATTAAATTAAATCT  60
              |||||| |||||||||||||||||||||||||| |||||  |||| ||| ||| |||||
Db   33  ATGAAAATTTAATATTTTAATATTTTGATTATTTTCCTTATTTTCCTTATTAATGAATTAAATCT  92

Qy   61  GCTAATTGTCCTGTTGGAACTGAAACTACCACAGCCGGATAAGTTGATGATCTAGGAACT  120
              |-||||||||| | ||||||||||||||||| ||||||| ||||||||||||| ||||
Db   93  GTTAATTGTCCTAATGTGCTGCAATTGCCAATTGGCAATAAFCTGATACAGGAGCTGCAGAT  152

Qy  121  CCTGCAAATTGTGTTAATTGTTAGAAAAACTTTTATTATAATAATAATGCTGCTGCT------  174
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Qy   153  ATAAATACTTGTACTCATTGCTAAAAACACTTTTACTTTAATGGTGGTAATCCTGCGACGT  212
               |||| ||||| |||| |||||||| |||||||||||||||| ||||| |||| ||||
Db   175  -----------------TTCGTTCCTGCTGCTAGTACGTGTACACCTTGTCCATAA  213

Qy   213  CAGGCTCCTGGTGCTGTACAATTCAATCCAGGTGTTAGTCAGTGCATAGCTTGCCAAGTA  272
               |||||||||||| |||| |||| ||| |||| |||||||||| |||||| ||||
Db   213  AAAAAAGATGCTGGTGCTGTAACCCTCCACCTGCTCCACTGCTACTGTCTAATTTAGTCACATAATGT  273

Qy   273  CACAAA---GCCGATTCTCAACACAGATAAGGTGGTGATGCTAATTTAGCCGCATAATGT  329

Qy   274  AACGTTAAATGCCCTGCTGGTACGGCAATTGCAGGTGGAGCAACAGATTATGCAGCAATA  333
               |||  |||  || ||||| ||||| |  |||||| |||| ||||| ||| ||| |||
Db   330  AGCAACTTATGTCCTGGCTGCCACTGCAGTTGAAGATGGATCACCTACTTTTACTTAATCC  389

Qy   334  ATCACAGAATGTGTTAATTGTAGAATTAATTTTATAAATGAAAATGCT  381
               |||||||| |||| ||||||||||| ||||||||||||||||
Db   390  CTCACATAATGTGTTAATTGTAAACCTAACTTTTACTTTAATGGTGGT  437
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RESULT 11
BQ134810
LOCUS   BQ134810   538 bp   mRNA   linear   EST 22-APR-2002
DEFINITION INIT1_4_C08.b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
           multifiliis cDNA, mRNA sequence.
ACCESSION BQ134810
VERSION   BQ134810.1 GI:20260909
KEYWORDS   EST.
SOURCE   Ichthyophthirius multifiliis.
ORGANISM   Ichthyophthirius multifiliis
           Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
           Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE 1 (bases 1 to 538)
AUTHORS   Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
           Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE   An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL   Unpublished (2002)
COMMENT   Contact: Cordonnier-Pratt MM
           Laboratory for Genomics and Bioinformatics
           The University of Georgia, Department of Plant Biology
           Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
           Tel: 706 542 1860
           Fax: 706 583 0210
           Email: mmpratt@uga.edu
           Sequences have been trimmed to exclude PolyA, vector, and regions
           below Phred quality 16. The threshold for highest quality sequence
           is 20.
           Seq primer: JEN REV
           High quality sequence stop: 531
           POLYA=No.
FEATURES   Location/Qualifiers
     source   1..538
                    /organism="Ichthyophthirius multifiliis"
                    /strain="G5"
                    /db_xref="taxon:5932"
                    /clone_lib="G5 trophont cDNA (INIT1)"
                    /note="Vector: pBluescript SK(-) from Lambda zap II;
                    Site_1: EcoRI; Site_2: EcoRI; The library was made from
                    trophont polyA+ RNA of the G5 parasite strain.
                    Double-stranded cDNA was linked to EcoRI adaptors, size
                    fractionated, and material >500 bp cloned into lambda ZAP
                    II. Plasmid DNA for sequencing was prepared by mass
                    excision."
BASE COUNT   155 a   101 c   106 g   175 t
ORIGIN

Query Match   8.1%; Score 113.8; DB 14; Length 538;
Best Local Similarity 59.2%; Pred. No. 1.4e-14;
Matches 234; Conservative   0; Mismatches 152; Indels   9; Gaps 2;

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Qy   171  TGCTTTCGTTCCTGGTGCTAGTACGTGTACACCTTGTCCATAAAAAAAAGATGCTGGTGC  230
               ||| |||||||||||||||||| ||  |||| || ||||||
Db   149  TCCTATGGTTCCTGGCCCTAATAGTAAATGCTAGCTTGCGAATCAAAAAAGACCAATTC  208
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Best Local Similarity   59.8%;   Pred. No. 7.6e-14;
Matches 239;   Conservative   0;   Mismatches 131;   Indels   30;   Gaps    2;

Qy    9  TAATATTTTAGTAATATTGATTATTTCATTATTTTCATTATTTTCATTAAATTAAATCTGCTAATTG  68
            ||||||||| || ||||| |||||||| ||||| ||| |||  |||   ||||||| ||||||
Db   14  TAATATTTTAATAATTTTGATTATTTCCTTATTTCCTATTTTATTAATAAGAGCTGTTAATTG   73

Qy   69  TCCTGTTGGAACTGAAACTAACACAGCCGGATAAGTTGATGATCTAGGAACTCCTGCAAA   128
            |||| |||  |   ||| |||||||||| ||||  || |||||||| ||||| ||||||
Db   74  TCCTAATGGTGCTGCAATTGCGAATGGTAATCTGATACAGGAGACTGCAGATATAAATAC   133

Qy  129  TTGTGGTAATTGTTAGAAAAACTTTATTATAATAAATGCTGCT-------            174
            |||| |||  || |||||||| |||||  |  ||  ||||| ||
Db  134  TTGTACTCATTGCTAAAAACACTTTTAATGGTGGTAATCCTGCAGGTCAGGCTCC      193

Qy  175  --------TTCGTTCCTGGTGCTAGTACGTTGTCAGTACCTTGTCGTCAGTACCAGTCAAAAAAAGA  221
                  ||||| ||||||  |||||| |||||| ||||| |||| |||| ||  |
Db  194  TGGTGCTGTACAATTCAATCCAGGTTGTTAGTCAGTTCAGTGCATAGCTTGCCAAGTACACAA--   251

Qy  222  TGCTGGTGCTTAACCAAATCCACCTGCTACTGCTAATTTAGTCACATATGTAACGTTAA      281
            |||| |||   |||||| |||| | |||| ||||| |||||| || |||||||||| |
Db  252  -GCCGATTCTCAACACAGATAAGGTGGTGATGCTAATTTAGCCGCATAATGTAGCCAACTT      310

Qy  282  ATGCCCTGCTGGTACCGCAATTGCAGGTGGAGCAACAGATTATGCAGCAATAATCACAGA  341
            || |||| || |||  || ||||| ||||| |||| |  |  | ||  ||||||| |||
Db  311  ATGTCCTGCTGCTGCACTGCAGTTGAAGCATGGATCACCTACTTTTACTTAATCCCTCACATA   370

Qy  342  ATGTGTTAATTGTAGAATTAATTTTTATATGAAAATGCT      381
            || |||  |||| ||| ||| |  || ||||| ||||||
Db  371  ATGTGTTAATTGTAAACCTAACTTTTTACTTTAATGGTGGT      410
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Qy  231  TTAACCAAATCCACCTGCTACTGCTAATTTAGTCACATAATGTAACGTTAAATGCCCTGC   290
            |||| ||  |||  | | ||||  |  |||||||| |||||||   | ||||  ||| |||
Db  209  TTAATTCCAGATCAGTCTTGAGGCTAATTTAGCCGCATAATGTGGCACTGGAATGTCCTGC   268

Qy  291  TGGTACCGCAATTGCAGGTGGAGCAACA--GATTATGCAGCAATAATCACAGAATGTGT   347
            ||||  || ||| || |||||  |||   ||| |||| |||||||| ||||||||||||
Db  269  TGGCACTCTTGTTACGAGCGAGTAACACCTACTTATACTGTATCACTCTCATAATGTGT   328

Qy  348  TAATTGTAGAATTAATTTTTTATAATGAAAAAATGTTTAATGCAGGTGCTAGTAC   407
            |||||| |||| || |||| |||||  |||| |||||   ||| |||| | | |||
Db  329  TAAATTGTAAAGCTGGCTTTTACTAAAATAGT-----AATTTCGAAGCAGGTAAAAGTTA   382

Qy  408  ATGCACAGCTTGTCCGGTAAACAGAGTTGTGGTGCATTGAACTGCTGGTAATGCCGCTAC   467
            |||| || |||  |||  |||| ||| ||| ||| ||| || | ||||||| ||||  |||
Db  383  ATGCAATAAGTGTGCAGTAAGTAAAACTGGTTCAGCATCGTTCCAGTAATAGTGTGCTAC   442

Qy  468  CATAGTTCGCATAATGTAACGTCGCGCATGTCCTACTGGTACTGCACTTGATGATGGAGTAAC   527
            || || |  ||||  || ||  ||| ||  | |  |||| |||  | ||| ||||| ||
Db  443  TTCAGCCACACAATGTGTAAAACGATTGCCCTGCCTGGTACAGTGGTTGATGATGTACATC   502

Qy  528  TACTGATTATGTTAGATCATTCACAGAATCTGTTA   562
            |||| |||| | ||||| ||| |||| |||| |||
Db  503  AACTAATTTTGTAGCTTTAGCAAGTGAAATGTACTA   537
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```
RESULT 12
BQ134905
LOCUS       BQ134905                 630 bp    mRNA    linear   EST 22-APR-2002
DEFINITION  INIT1_F04.b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
            multifiliis cDNA, mRNA sequence.
ACCESSION   BQ134905
VERSION     BQ134905.1  GI:20261004
KEYWORDS    EST.
SOURCE      Ichthyophthirius multifiliis.
  ORGANISM  Ichthyophthirius multifiliis
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE   1  (bases 1 to 630)
  AUTHORS   Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
            Dickerson,H., Lin,T.-L. and Pratt,L.H.
  TITLE     An EST database for Ichthyophthirius multifiliis (G5 isolate)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector, and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Seq primer: JEN REV
            High quality sequence stop: 629
            POLYA=NO.
FEATURES             Location/Qualifiers
     source          1..630
                     /organism="Ichthyophthirius multifiliis"
                     /strain="G5"
                     /db_xref="taxon:5932"
                     /clone_lib="G5 trophont cDNA (INIT1)"
                     /note="Vector: pBluescript SK(-) from Lambda Zap II;
                     Site_1: EcoRI; Site_2: EcoRI; The library was made from
                     trophont polyA+ RNA of the G5 parasite strain.
                     Double-stranded cDNA was linked to EcoRI adaptors, size
                     fractionated, and material >500 bp cloned into lambda ZAP
                     II. Plasmid DNA for sequencing was prepared by mass
                     excision."
BASE COUNT      179 a    120 c    118 g    213 t
ORIGIN

Query Match     7.9%;  Score 110.4;  DB 14;  Length 630;
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RESULT 13
BQ134827
LOCUS       BQ134827                 631 bp    mRNA    linear   EST 22-APR-2002
DEFINITION  INIT1_4_E06.b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
            multifiliis cDNA, mRNA sequence.
ACCESSION   BQ134827
VERSION     BQ134827.1  GI:20260926
KEYWORDS    EST.
SOURCE      Ichthyophthirius multifiliis.
  ORGANISM  Ichthyophthirius multifiliis
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE   1  (bases 1 to 631)
  AUTHORS   Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
            Dickerson,H., Lin,T.-L. and Pratt,L.H.
  TITLE     An EST database for Ichthyophthirius multifiliis (G5 isolate)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector, and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Seq primer: JEN REV
            High quality sequence stop: 630
            POLYA=NO.
FEATURES             Location/Qualifiers
     source          1..631
                     /organism="Ichthyophthirius multifiliis"
                     /strain="G5"
                     /db_xref="taxon:5932"
                     /clone_lib="G5 trophont cDNA (INIT1)"
                     /note="Vector: pBluescript SK(-) from Lambda Zap II;
                     Site_1: EcoRI; Site_2: EcoRI; The library was made from
                     trophont polyA+ RNA of the G5 parasite strain,
                     Double-stranded cDNA was linked to EcoRI adaptors, size
                     fractionated, and material >500 bp cloned into lambda ZAP
```

II. Plasmid DNA for sequencing was prepared by mass
    excision."

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BASE COUNT      180 a      120 c      118 g      213 t
ORIGIN
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Query Match
Best Local Similarity   7.9%;   Score 110.4; DB 14; Length 631;
Matches 239; Conservative 0; Mismatches 131; Indels 30; Gaps 2;
                                               Pred. No. 7.6e-14;

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Qy    9  TAATATTTTAGTAATATTGATTATTTCATTATTTATCAATTAAAATTAAATCTGCTAATTG  68
            ||||||| |||| ||||||| ||||||||| ||| || ||| ||| |||  |||||
Db   15  TAATATTTTAATAATTTTGATTATTTCCTTATTTATTATTAATGAATTAAGAGCTGTTAATTG  74

Qy   69  TCCTGTTGGAACTGAAACTAACACAGCCGATAAGTTGATGATCTAGGAACTCCTGCAAA  128
            |||| |  |  |||||||   ||  || |||||| | | |  | |
Db   75  TCCTAATGGTGCTGCAATTGCCAATCTGATAATCTGCAGATATAAATAC  134

Qy  129  TTGTGTTAATTGTTAGAAAAACTTTTATTATTATAATATGCTGCT---------  174
            ||| | |||| ||| || |||||| ||||||| ||||||  |
Db  135  TTGTACTCATTGCTAAAAACACTTTACTTTAATGGTGGTAATCCTGCAGGTCAGGCTCC  194

Qy  175  ----------TTCGTTCCTGGTTGCTAGTACGTTGTACACCTTGTCCATAAAAAAGA  221
                    ||| ||||| ||| | |||||||  ||  |||
Db  195  TGGTGCTGTACAATTCAATCCAGGTGTTAGTCAGTGCATAGCTTGCCAAGTACCACAAA--  252

Qy  222  TGCTGGTGCTTAACCAAATCCACCTGCTACTGCTAATTTAGTCACATAATGTACGTTAA  281
            |  |||  ||| |||  |  |||| |||| ||||| |||||| ||||
Db  253  -GCCGATTCTCAACACAGATAAGGTGGTGATGCTAATTTAGCCGCATAATGTACCAACTT  311

Qy  282  ATGCCCTGCTGGTACCGCAATTGCAGTGGAGCAACAGATTATGCAGCAATATCACAGA  341
            ||| ||||| ||| |||  ||| |  |||||| |||| | ||  || ||||  | |
Db  312  ATGTCCGTCGTGGCACTGCAGTTGAAGATGGATCACCCTCTTAATCCCTCACATA  371

Qy  342  ATGTGTTAATTGTAGAATTAATTTTTATAATGAAAATGCT  381
            ||||||||||||| |||   || ||  |  | |||||| |
Db  372  ATGTGTTAATTGTAAACCTAACTTTTACTTTAATGGTTGGT  411
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```
RESULT 14
BQ134970
LOCUS        BQ134970              523 bp    mRNA    linear   EST 22-APR-2002
DEFINITION   INIT1_2_D10.b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
             multifiliis cDNA, mRNA sequence.
ACCESSION    BQ134970
VERSION      BQ134970.1  GI:20261069
KEYWORDS     EST.
SOURCE       Ichthyophthirius multifiliis.
  ORGANISM   Ichthyophthirius multifiliis
             Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
             Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE    1  (bases 1 to 523)
  AUTHORS    Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
             Dickerson,H., Lin,T.-L. and Pratt,L.H.
  TITLE      An EST database for Ichthyophthirius multifiliis (G5 isolate)
  JOURNAL    Unpublished (2002)
COMMENT      Contact: Cordonnier-Pratt MM
             Laboratory for Genomics and Bioinformatics
             The University of Georgia, Department of Plant Biology
             Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
             Tel: 706 542 1860
             Fax: 706 583 0210
             Email: mmpratt@uga.edu
             Sequences have been trimmed to exclude PolyA, vector, and regions
             below Phred quality 16. The threshold for highest quality sequence
             is 20.
             Seq primer: JEN REV
             High quality sequence stop: 508
             POLYA=No.
FEATURES             Location/Qualifiers
     source          1..523
                     /organism="Ichthyophthirius multifiliis"
                     /strain="G5"
                     /db_xref="taxon:5932"
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/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."

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BASE COUNT      147 a       98 c       99 g      179 t
ORIGIN
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Query Match
Best Local Similarity   7.8%;   Score 109.4; DB 14; Length 523;
Matches 238; Conservative 0; Mismatches 131; Indels 30; Gaps 2;
                                               Pred. No. 1.2e-13; Similarity 59.6%;

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Qy   10  AATATTTTAGTAATATTGATATTCATTATTTATCAATTAAATTAAATCTGCTAATTGT  69
            ||||||| ||||| ||||  |||||||| ||| ||| ||| |||  ||||||||
Db   12  AATATTTTAATAATTTTGATTATTTCCTTATTTATTAATGAATTAAGAGCTGTTAATTGT  71

Qy   70  CCTGTTGGAACTGAAACTAACAGCCGGATAAGTTGATGATCTAGGAACTCCTGCAAAT  129
            ||| | ||  | ||||||  | | ||| |||||| | | | |  |
Db   72  CCTAATGGTGCTGCAATTGCCAATCTGATAATCTGCAGATATAAATACT  131

Qy  130  TGTGTTAATTGTTAGAAAAACTTTTATTATTATAATAATGCTGCTGCT----------  174
            |||||||| ||||||  |||| | ||||||||  | |
Db  132  TGTACTCATTGCTAAAAACACTTTACTTTAATGGTGGTAATCCTGCAGTTCAGGCTCCT  191

Qy  175  ----------TTCGTTCCTGGTTGCTAGTACGTTGTACACCTTGTCCATAAAAAAGAT  222
                    ||| | ||| ||  |||||||  ||| |||
Db  192  GGTGCTGTACAATTCAATCCAGGTGTTAGTCAGTGCATAGCTTGCCAAGTACCACAAA---  248

Qy  223  GCTGGTGCTTAACCAAATCCACCTGCTACTGCTAATTTAGTCACATAATGTACGTTAAA  282
            |  |||  ||| ||||  |  |||| |||  |||| ||||| ||||
Db  249  GCCGATTCTCAACACAGATAAGGTGGTGATGCTAATTTAGCCGCATAATGTAGCAACTTA  308

Qy  283  TGCCCTGCTGGTACCGCAATTGCAGTGGAGCAACAGATTATGCAGCAATAATCACAGAA  342
            ||| ||||| ||| ||  |||| | |||||| | || | |  || |||| |  | |
Db  309  TGTCCTGCTGCACTGCAGTTGAAGATGGATCACCCTACTTTTACTTAATCCCTCACATAA  368

Qy  343  TGTGTTAATTGTAGAATTAATTTTTATAATGAAAATGCT  381
            |||||||||||| ||  || ||| ||  | |||||| |
Db  369  TGTGTTAATTGTAAACCTAACTTTTACTTTAATGGTGGT  407
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```
RESULT 15
BQ134761/c
LOCUS        BQ134761              514 bp    mRNA    linear   EST 22-APR-2002
DEFINITION   INIT1_3_F07.b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
             multifiliis cDNA, mRNA sequence.
ACCESSION    BQ134761
VERSION      BQ134761.1  GI:20260860
KEYWORDS     EST.
SOURCE       Ichthyophthirius multifiliis.
  ORGANISM   Ichthyophthirius multifiliis
             Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
             Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE    1  (bases 1 to 514)
  AUTHORS    Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
             Dickerson,H., Lin,T.-L. and Pratt,L.H.
  TITLE      An EST database for Ichthyophthirius multifiliis (G5 isolate)
  JOURNAL    Unpublished (2002)
COMMENT      Contact: Cordonnier-Pratt MM
             Laboratory for Genomics and Bioinformatics
             The University of Georgia, Department of Plant Biology
             Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
             Tel: 706 542 1860
             Fax: 706 583 0210
             Email: mmpratt@uga.edu
             Sequences have been trimmed to exclude PolyA, vector, and regions
             below Phred quality 16. The threshold for highest quality sequence
             is 20.
             Seq primer: JEN REV
             High quality sequence stop: 502
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FEATURES             Location/Qualifiers
     source          1..514
                     /organism="Ichthyophthirius multifiliis"
                     /strain="G5"
                     /db_xref="taxon:5932"
                     /clone_lib="G5 trophont cDNA (INIT1)"
                     /note="Vector: pBluescript SK(-) from Lambda Zap II;
                     Site_1: EcoRI; Site_2: EcoRI; The library was made from
                     trophont polyA+ RNA of the G5 parasite strain.
                     Double-stranded cDNA was linked to EcoRI adaptors, size
                     fractionated, and material >500 bp cloned into lambda ZAP
                     II. Plasmid DNA for sequencing was prepared by mass
                     excision."
POLYA=No.

BASE COUNT      166 a        96 c       102 g       149 t       1 others
ORIGIN

Query Match           7.6%;    Score 106.4; DB 14;  Length 514;
Best Local Similarity 60.8%;   Pred. No. 5.6e-13;
Matches  192; Conservative   0; Mismatches  121;    Indels    3;  Gaps      1;

Qy   366 TTATAATGAAAATGCTCCAAATTTTAATGCAGGTGCTAGTACATGCACAGCTTGTCCGGT 425
             | |||||   | ||| |||  | | |  | ||  |   |||| | ||||||   ||
Db   431 TAATAATCCTGAAGTTCCTAATGTTTCTAGCCCTAATGTTAATGCGTAGCTTGCTAAGT 372

Qy   426 AAACAGAGTTGGTGGTGCATTGACTTGCTGGTAATGCCGCTACCATAGTCGCATAATGTAA 485
             |||||   ||  |  |   | |||  |||    |||| ||| |||||||||||
Db   371 AAACAAGTCTGATTCCAATTAAGACCAGGTGCTTAGGCTAATTTAGCCACACATAAIGTAA 312

Qy   486 CGTCGCATGTCCTACTGGTACTGCCACTTGATGATGGAGTAACTACTGATTATGTTAGATC 545
             | |||||||||||||||||||||| || | || || | |  ||||| | || |||
Db   311 CAATGAATGTCCCACTGGCACTGCTATTCAAGACGGAGCAATATTTATTTATACTTAATC 252

Qy   546 ATTCACAGAAATGTGTTAAATGTAGACTTAACTTTACTATAATGGTAATAATGGTAATAC 605
             | ||| ||||   | ||| ||| || ||||||||||  ||||||| || | | | |
Db   251 AATCTCATAATGTACTTTTGTAAAGTTGACTTTTTACTTTAATGGTGGCAA--TCCTTC 195

Qy   606 TCCTTTCAATCCAGGTAAAAGTTAATGCACACCTTGTCCGGCAATTAAACCTGCTAATGT 665
             || |||||||||| ||||| | |||| ||| |  | | | || ||| |||||||
Db   194 AGCTCAGAATCCTGGTAATGGATAAATCACTCCAGGTAATTGATTGCAAATCCTGATGC 135

Qy   666 TGCTTAAGCTACTTTA 681
             |||| |||| |||
Db   134 TGCTACTGCTGCTTAA 119
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